SEQUENCE LISTING

<110> Lovejoy, David

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Barsyte, Dalia

Rotzinger, Susan

<120> Tereuin C-Terminal Associated Peptides (TCAP) And Methods And Uses Thereof

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<150> US 60/376,879

<151> 2002-05-02

<150> US 60/377,231

<151> 2002-05-03

<150> US 60/424,016

<151> 2002-11-06

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Asn Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Ala Lys Ser Leu Ile 35 40 45

Gly Lys Gly Val Met Leu Ala Val Thr Gln Gly Arg Val Val Thr Asn 50 55 60

Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly Arg 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu Gly
100 105 110

Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val Asn 115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg 130 135 140

Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val Arg 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln Ala 165 170 175

Arg Gln Lys Ala Leu Ser Ser Ala Trp Ser Arg Glu Gln Gln Arg Val 180 185 190

Arg Glu Gly Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys Arg 195 200 205

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val 210 215 220

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile 225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg

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Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Gln Tyr Asn Glu Gly Arg
20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val 35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Glu Gly Ile Val Thr Ala 50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile 65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu 100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Ile Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg 130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile 145 150 155 160 Arg Tyr Gly Thr Thr Val Glu Glu Lys Asn His Val Leu Glu Met 165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Gln Glu Gln Arg Arg 180 185 190

Leu Gln Glu Gly Glu Gly Thr Arg Val Trp Thr Glu Gly Glu Lys 195 200 205

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe 210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn 225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg 245 250

<210> 5

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M2

<400> 5

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Leu Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile 20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly 35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val 50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn 65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp 85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ala Ala Asp Gly Asp Leu Val Thr 100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe 130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Ser Ile Arg Tyr 145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp 165 170 175

Gln Ala Gly Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln 180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr 210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser 225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg 245 250

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<223> Mouse Ten M3

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Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Lys Ala 20 25 30

Gly Ala Glu Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile 35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn 50 60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Pro Glu Ser Asp Leu Gly 100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn 115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg 130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala 165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val 180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg 195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val 210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile

225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg 245 250

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<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M4

<400> 7

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Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser 20 25 30

Cys Gln Gln Ala Pro Glu Thr Lys Lys Phe Ala Ser Ser Gly Ser Ile 35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr 50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Ile Ala Ala Ile 65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu 100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Met Leu Ile Gln Leu Gln Tyr 130 135 140 Lys Val Arg Val Leu Glu Leu Ala Arg Gln Arg Ala Val Arg Gln Ala 165 170 175

Trp Ala Arg Glu Gln Gln Arg Leu Arg Glu Glu Glu Glu Gly Leu Arg
180 185 190

Ala Trp Thr Asp Gly Glu Lys Gln Gln Val Leu Asn Thr Gly Arg Val 195 200 205

Gln Gly Tyr Asp Gly Phe Phe Val Thr Ser Val Glu Gln Tyr Pro Glu 210 . 215 220

Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Met 225 230 235 240

Gly Arg Arg

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<212> PRT

<213> Artificial Sequence

<220>

<223> Human Ten M1

<400> 8

Thr Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe 1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg 20 25 30

Cys Leu Glu Gly Cly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val 35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala 50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile 65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu 100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Ile Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg 130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile 145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Lys Asn His Val Leu Glu Ile 165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg 180 185 190

Leu Gln Glu Gly Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys 195 200 205

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe 210 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn 225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg 245 250

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<223> Human Ten M2

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Met Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile 20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly 35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val 50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn 65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp 85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ser Ala Asp Gly Asp Leu Val Thr 100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val 115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe 130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr 145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp 165 170 175

Gln Ala Arg Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln 180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu 195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr

210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser 225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg 245 250

<210> 10

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Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Ala 20 25 30

Gly Gly Ala Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn 50 55 60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Pro Glu Ser Asp Leu Gly
100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn 115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg 130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala 165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val 180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg 195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val 210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile 225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg 245 250

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Cys Leu Gln Ala Pro Lys Thr Lys Lys Phe Ala Ser Ser Gly Ser Val\$35\$ 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr 50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Val Ala Ala Ile 65 70 75 80

Leu Asn His Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu
100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Val Leu Ser Gly Arg Thr Arg 130 135 140

Arg Tyr Thr Asp Ile Gln Leu Gln Tyr Gly Ala Leu Cys Leu Asn Thr 145 150 155 160

Arg Tyr Gly Thr Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Leu 165 170 175

Ala Arg Gln Arg Ala Val Arg Gln Ala Trp Ala Arg Glu Gln Gln Arg 180 185 190

Leu Arg Glu Gly Glu Gly Leu Arg Ala Trp Thr Glu Gly Glu Lys
195 200 205

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe 210 215 220

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn 225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg 245 250

<210> 12

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish Ten M3

<400> 12

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Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser 20 25 30

Ser Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Gly Lys Gly Val Met Leu Ala Ile Thr Ser Lys Gly Gln Val Ala Thr 50 55 60

Asn Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Val Thr Val 65 70 75 80

Leu Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu 100 105 110

Gly Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg 130 135 140

Arg Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val 145 150 155 160

Arg Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln 165 170 175

Ala Arg Gln Arg Ala Leu Ser Ser Ala Trp Ala Arg Glu Gln Gln Arg 180 185 190

Val Arg Asp Gly Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys

195 200 205 Arg Gln Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr 215 Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn 225 230 235 240 Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg 245 <210> 13 <211> 40 <212> PRT <213> Artificial Sequence <220> <223> Rainbow Trout TCAP3 (40a.a.) <400> 13 Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile Gln Phe Leu Arg Gln Ser Glu Ile

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<211> 41

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<223> Rainbow Trout TCAP 3 (41a.a.)

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Arg Gln Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr

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15

<400> 16

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cagtaccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata	120
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	132
atagggaaga gg	132
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<212> PRT	
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Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val 20 25 30	

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<211> 41
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<213> Artificial Sequence
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<223> Zebrafish TCAP3 (41 a.a.)
<400> 22
Arg Gln Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
Val Gln Phe Leu Arg Gln Ser Glu Ile
<210> 23
<211> 43
<212> PRT
<213> Artificial Sequence
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<223> Zebrafish preTCAP3 (43 a.a.)
<400> 23
Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val
Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
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Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
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caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata
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gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag
                                                                   120
                                                                   123
ata
<210> 27
<211> 129
<212> DNA
<213> Artificial Sequence
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caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata
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gggaagagg
<210> 28
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<212> DNA
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gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag
                                                                   120
                                                                    132
atagggaaga gg
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<210> 29

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<211> 40
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<223> Zebrafish TCAP4 (40 a.a.)
<400> 29
Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile
                                 10
Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val
                        25
       20
His Phe Trp Arg Gln Thr Glu Met
<210> 30
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Zebrafish TCAP4 (41 a.a.)
<400> 30
Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
               5
                                                      15
Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
           20
                              25
                                              30
Val His Phe Trp Arg Gln Thr Glu Met
       35
<210> 31
<211> 43
<212> PRT
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<213> Artificial Sequence
<220>
<223> Zebrafish preTCAP4 (43 a.a.)
<400> 31
Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile
Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val
           20
                               25
His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
<210> 32
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Zebrafish preTCAP4 (44 a.a.)
<400> 32
Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
                                25
           20
Val His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
        35
                            40
<210> 33
<211> 120
<212> DNA
<213> Artificial Sequence
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<220> <223> Zebrafish TCAP4 (120 n.a.) cagetectaa getetggaeg tgtacaggge tacgaagget tetacatagt atcagtegae 60 cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120 <210> 34 <211> 123 <212> DNA <213> Artificial Sequence <220> <223> Zebrafish TCAP4 (123 n.a.) 60 cagcagetee taagetetgg acgtgtacag ggetacgaag gettetacat agtateagte gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120 123 atg <210> 35 <211> 129 <212> DNA <213> Artificial Sequence <220> <223> Zebrafish preTCAP4 (129 n.a.) <400> 35 cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60 cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120 129 ggacgcagg <210> 36

<211> 132

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<212> DNA
<213> Artificial Sequence
<220>
<223> Zebrafish preTCAP4 (132 n.a.)
<400> 36
                                                                    60
cagcagetee taagetetgg aegtgtacag ggetacgaag gettetacat agtateagte
                                                                    120
gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag
atgggacgca gg
                                                                    132
<210> 37
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP1 (40 a.a.)
<400> 37
Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
His Phe Met Arg Gln Ser Glu Ile
        35
<210> 38
<211> 41
<212> PRT
<213> Artificial Sequence
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<220>

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<223> Mouse TCAP1 (41 a.a.)
<400> 38
Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
                             25
Ile His Phe Met Arg Gln Ser Glu Ile
<210> 39
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP1 (43 a.a.)
<400> 39
Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
               5
Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
       35
                           40
<210> 40
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP1 (44 a.a.)
<400> 40
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Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg <210> 41 <211> 120 <212> DNA <213> Artificial Sequence <220> <223> Mouse TCAP1 (120 n.a.) <400> 41 cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60 cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata 120 <210> 42 <211> 123 <212> DNA <213> Artificial Sequence <220> <223> Mouse TCAP1 (123 n.a.) <400> 42 60 cagcagcttt tgggcaccgg gagggtgcag gggtatgatg ggtattttgt cttgtctgtt gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa 120 123 ata <210> 43

<211> 129

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<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP1 (129 n.a.)
<400> 43
cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag
                                                                    60
cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata
                                                                    120
ggcaggagg
                                                                    129
<210> 44
<211> 132
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP1 (132 n.a.)
<400> 44
cagcagcttt tgggcaccgg gagggtgcag gggtatgatg ggtattttgt cttgtctgtt
                                                                   60
gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa
                                                                    120
                                                                    132
ataggcagga gg
<210> 45
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223>
      Mouse TCAP2 (40 a.a.)
<400> 45
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
               5
                                                       15
```

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Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
Gln Phe Leu Arg Gln Asn Glu Ile
<210> 46
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP2 (41 a.a.)
<400> 46
Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Asn
                               25
           20
Ile Gln Phe Leu Arg Gln Asn Glu Met
<210> 47
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP2 (43 a.a)
<400> 47
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
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25

20

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Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
<210> 48
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP2 (44 a.a.)
<400> 48
Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
<210> 49
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP2 (120 n.a.)
<400> 49
caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa
                                                                   60
cagtacccgg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagagg
                                                                    120
<210> 50
<211> 123
<212> DNA
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<213> Artificial Sequence <220> <223> Mouse TCAP 2 (123 n.a.) <400> 50 cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60 gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120 atg 123 <210> 51 <211> 129 <212> DNA <213> Artificial Sequence <220> <223> Mouse preTCAP2 (129 n.a.) <400> 51 caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa 60 cagtacccgg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagatg 120 129 ggaaagagg -<210> 52 <211> 132 <212> DNA <213> Artificial Sequence <220> <223> Mouse preTCAP2 (132 n.a.) <400> 52 cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60 gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120 atgggaaaga gg 132

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<210> 53
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP3 (40 a.a.)
<400> 53
Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
Gln Phe Leu Arg Gln Ser Glu Ile
<210> 54
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP3 (41 a..a)
<400> 54
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
                5
                                                       15
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
           20
                               25
Ile Gln Phe Leu Arg Gln Ser Glu Ile
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<210> 55

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<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP3 (43 a.a.)
<400> 55
Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
                                   10
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
                               25
Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
<210> 56
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP3 (44 a.a.)
<400> 56
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
                                   10
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
        20
                               25
Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
<210> 57
<211> 120
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<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP3 (120 n.a.)
<400> 57
cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag
                                                                   60
cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc
                                                                   120
<210> 58
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP3 (123 n.a.)
<400> 58
cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcggtg 60
gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag
                                                                   120
                                                                   123
atc
<210> 59
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP3 (129 n.a.)
<400> 59
cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag
                                                                   60
cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc
                                                                   120
                                                                   129
ggcaagagg
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<210> 60
<211> 132
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP3 (132 n.a.)
<400> 60
cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcggtg
                                                                     60
gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag
                                                                    120
atcggcaaga gg
                                                                    132
<210> 61
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP4 (40 a.a.)
<400> 61
Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
           20
                               25
His Phe Met Arg Gln Ser Glu Met
        35
<210> 62
<211> 41
<212> PRT
<213> Artificial Sequence
```

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<220>
<223> Mouse TCAP4 (41 a.a.)
<400> 62
Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
                              25
Ile His Phe Met Arg Gln Ser Glu Met
<210> 63
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP4 (43 a.a.)
<400> 63
Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
   20
                               25
His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
       35
<210> 64
<211> 44
<212> PRT
<213> Artificial Sequence
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<220>

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<223> Mouse preTCAP4 (44 a.a.)
<400> 64
Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
                               25
Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
       35
                           40
<210> 65
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP4 (120 n.a.)
<400> 65
caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag
                                                                   60
                                                                    120
cagtacccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg
<210> 66
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP4 (123 n.a.)
<400> 66
cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc
                                                                    60
gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag
                                                                    120
                                                                    123
atg
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<210> 67
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP4 (129 n.a.)
<400> 67
caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag
                                                                   60
cagtacccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg
                                                                   120
                                                                   129
ggccgaagg
<210> 68
<211> 132
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP4 (132 n.a.)
<400> 68
cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc
                                                                   60
                                                                    120
gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag
                                                                    132
atgggccgaa gg
<210> 69
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Human TCAP1 (40 a.a.)
<400> 69
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Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Ile <210> 70 <211> 41 <212> PRT <213> Artificial Sequence <220> <223> Human TCAP1 (41 a.a.) <400> 70 Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Ile 35 <210> 71 <211> 43 <212> PRT <213> Artificial Sequence <220> <223> Human preTCAP1 (43 a.a.) <400> 71 Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val 10

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile

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His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
<210> 72
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Human preTCAP1 (44 a.a.)
<400> 72
Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
                               25
Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
<210> 73
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP1 (120 n.a.)
cagcttttga gcactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag
                                                                   60
cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata
<210> 74
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<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP1 (123 n.a.)
<400> 74
cagcagettt tgagcactgg gegggtacaa ggttacgatg ggtattttgt tttgtctgtt
                                                                    60
gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa
                                                                    120
                                                                    123
ata
<210> 75
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223> Human preTCAP1 (129 n.a.)
<400> 75
cagcttttga gcactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag
                                                                    60
cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata
                                                                    120
                                                                    129
ggcaggagg
<210> 76
<211> 132
<212> DNA
<213> Artificial Sequence
<220>
<223> Human preTCAP1 (132 n.a.)
<400> 76
cagcagettt tgagcactgg gegggtacaa ggttacgatg ggtattttgt tttgtctgtt
                                                                     60
```

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gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa
                                                                    120
ataggcagga gg
                                                                    132
<210> 77
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Human TCAP2 (40 a.a.)
<400> 77
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
Gln Phe Leu Arg Gln Asn Glu Met
<210> 78
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Human preTCAP2 (41 a.a.)
<400> 78
Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
                5
                                                       15
Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
            20
                               25
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Ile Gln Phe Leu Arg Gln Asn Glu Met

35 40

<210> 79

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (43 a.a.)

<400> 79

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val 1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile 20 25 30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg 35 40

<210> 80

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (44 a.a.)

<400> 80

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr 1 5 10 15

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
35 40

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<210> 81
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP2 (120 n.a.)
<400> 81
cagettetga geacegggeg egtgeaaggg taegagggat attaegtget teeegtggag
                                                                     60
caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg
                                                                    120
<210> 82
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP2 (123 n.a.)
<400> 82
cagcagcttc tgagcaccgg gcgcgtgcaa gggtacgagg gatattacgt gcttcccgtg
                                                                    60
gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag
                                                                    120
atg
                                                                    123
<210> 83 .
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223> Human preTCAP2 (129 n.a.)
<400> 83
cagettetga geaceggeg egtgeaaggg taegagggat attaegtget teeegtggag
                                                                     60
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caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg
                                                                     120
ggaaagagg
                                                                     129
<210> 84
<211> 132
<212> DNA
<213> Artificial Sequence
<220>
<223> Human preTCAP2 (132 n.a.)
<400> 84
cagcagette tgagcacegg gegegtgeaa gggtacgagg gatattacgt getteeegtg
                                                                      60
                                                                     120
gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag
                                                                     132
atgggaaaga gg
<210> 85
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Human TCAP3 (40 a.a.)
<400> 85
Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
                                25
          - 20
Gln Phe Leu Arg Gln Ser Glu Ile
        35
<210> 86
<211> 41
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<212> PRT
<213> Artificial Sequence
<220>
<223> Human TCAP3 (41 a.a.)
<400> 86
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
                          10
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
                             25
Ile Gln Phe Leu Arg Gln Ser Glu Ile
<210> 87 .
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Human preTCAP3 (43 a.a.)
<400> 87
Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
               5
                                                      15
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
                              25
           20
Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
       35
                           40
<210> 88
<211> 44
<212> PRT
<213> Artificial Sequence
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<220>
<223> Human preTCAP3 (44 a.a.)
<400> 88
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
                               25
Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
<210> 89 .
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP3 (120 n.a.)
<400> 89
cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag
cagtaccccg agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc
                                                                   120
<210> 90
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP3 (123 n.a.)
<400> 90
cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggtg
                                                                    60
                                                                   120
gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag
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atc		123
<210>	91	
<211>	129	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Human preTCAP (129 n.a.)	
<400>	91 ctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag	60
	cccg agctggccga cagcgccaac aacatccagt teetgeggca gagegagate	120
		129
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His Phe Met Arg Gln Ser Glu Met
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Ile His Phe Met Arg Gln Ser Glu Met
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<223> Human preTCAP4 (43 a..a)
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atg						123
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20 25 30

Val His Phe Trp Arg Gln Thr Glu Met
35 40

<210> 103

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<212> PRT

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<223> D. melanogaster Ten-m gene product

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Glu Leu Val Gln His Gly Asp Val Asp Gly Trp Asn Gly Asp Ile His 1 5 10 15

Ser Ile His Lys Tyr Pro Gln Leu Ala Asp Pro Gly Asn Val Ala Phe $20 \hspace{1cm} 25 \hspace{1cm} 30$

Gln Arg Asp Ala Lys 35

<210> 104

<211> 41

<212> PRT

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<223> Human CRF TCAP like region

<400> 104

Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg 1 5 10 15

Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His 20 2530

Ser Asn Arg Lys Leu Met Glu Ile Ile 35 40

<210> 105

<211> 40

<212> PRT

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<220>

<223> Human urocortin TCAP-like region

<400> 105

Asp Asn Pro Ser Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr 1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln 20 25 30

Asn Arg Ile Ile Phe Asp Ser Val 35 40

<210> 106

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Human urocortin 2 TCAP-like region

<400> 106

Ile Val Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Gln Ile Leu Leu 1 5 10 15

Glu Gln Ala Arg Ala Arg Ala Ala Arg Glu Gln Ala Thr Thr Asn Ala 20 25 30

Arg Ile Leu Ala Arg Val

<210> 107

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Human urocortin 3 TCAP=like region

<400> 107 ·

Phe Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Leu Leu Phe 1 5 10 15

Asn Ile Ala Lys Ala Lys Asn Leu Arg Ala Gln Ala Ala Asn Ala 20 25 30

His Leu Met Ala Gln Ile 35

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<211> 46

<212> PRT

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<223> L. migratoria DP

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Met Gly Met Gly Pro Ser Leu Ser Ile Val Asn Pro Met Asp Val Leu 1 5 10 15

Arg Gln Arg Leu Leu Glu Ile Ala Arg Arg Arg Leu Arg Asp Ala 20 25 30

Glu Glu Gln Ile Lys Ala Asn Lys Asp Phe Leu Gln Gln Ile 35 40 45

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<223> A. domesticus DP

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Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg
1 5 10 15

Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln 20 25 30

Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile 35 40 45

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<223> T. molitor DP

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Ser Pro Thr Ile Ser Ile Thr Ala Pro Ile Asp Val Leu Arg Lys Thr 1 5 10 15

Trp Glu Glu Arg Ala Arg Lys Gln Met Val Ala Gln Asn Arg 20 25 30

Glu Phe Leu Asn Ser Leu Asn 35

<210> 111

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<223> M. sexta DP-1

<400> 111

Arg Met Pro Ser Leu Ser Ile Asp Leu Pro Met Ser Val Leu Arg Gln 1 5 10 15

Lys Leu Ser Leu Glu Lys Glu Arg Lys Val His Ala Leu Arg Ala Ala 20 25 30

Ala Asn Arg Asn Phe Leu Asn Asp Ile 35 40

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Ser Leu Ser Val Asn Pro Ala Val Asp Ile Leu Gln His Arg Tyr Met 1 5 10 15

Glu Lys Val Ala Gln Asn Asn Arg Asn Phe Leu Asn Arg Val 20 25 30

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<223> P. Americana

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Gln Asp Gln Ile Gln Asn Arg Glu Ile Leu Gln Thr Ile 35 40 45

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<211> 41

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<223> O. keta CRP

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Gln Met Asn Glu Met Ser Arg Ala Glu Gln Leu Gln Gln Gln Ala His $20 \hspace{1cm} 25 \hspace{1cm} 30$

Ser Asn Arg Lys Met Met Glu Ile Phe 35 40

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<223> R. norvegicus

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Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln 20 25 30

Asn Arg Ile Ile Phe Asp Ser Val 35 40

<210> 116

<211> 37

<212> PRT

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<223> P. sauvageii

<400> 116

Gln Gly Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys 1 5 10 15

Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala As
n 20 25 30

Asn Arg Leu Leu Leu 35

<210> 117

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<223> C. carpio US

<400> 117

Asn Asp Asp Pro Pro Ile Ser Ile Asp Leu Thr Phe His Leu Leu Arg
1 5 10 15

Asn Met Ile Glu Met Ala Arg Asn Glu Asn Gln Arg Glu Gln Ala Gly

Leu Asn Arg Lys Tyr Leu Asp Glu Val 35 40

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<223> M. Musculus UCN2

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Glu Gln Ala Arg Tyr Lys Ala Ala Arg Asn Gln Ala Ala Thr Asn Ala 20 25 30

Gln Ile Leu Ala His Val

<210> 119

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<223> R. dano UCN2

<400> 119

Leu Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Val Leu Phe 1 5 10 15

Asp Val Ala Lys Ala Lys Asn Leu Arg Ala Lys Ala Ala Glu Asn Ala

Arg Leu Leu Ala His Ile 35	
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agccaacgcg agcgagcaga gcagaaccga atcatactca acgcggtggg caagtgatcg	180
gcccggtgtg ggaccccaaa aggctcgacc ctttccccta cctaccccgg ggctgaagtc	240
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<223> X=I or L
<220>
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<223> X=L, I or F

<222> (2)..(2)

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<222> (3)..(3)
<223> X=E, N, S or P
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tgt gcg gaa atg ggg ctc cct cac aga ggt tac tcc atc agt gca ggg

Cys Ala Glu Met Gly Leu Pro His Arg Gly Tyr Ser Ile Ser Ala Gly

394

100					105					110					115	
	gat Asp														gcc Ala	442
	aga Arg								_		_			_	_	490
	agc Ser															538
	agg Arg 165	_				_										586
	acc Thr	_	_		_	_				_	_		_		_	634
	cac His	_							_			_			_	682
	aac Asn	_	-	_	-	_	_	_	_	_		_		_		730
	aca Thr				_	_	_	_	_	-		-			_	778
	gta Val 245				_											826
	acg Thr															874
	tct Ser															922
	aga Arg	-	_				_	_			_		_	_		970
	tgc Cys															1018
	ctc Leu 325					_	_									1066
tta	cag	cag	acg	gaa	aat	gac	aca	ttc	gag	aat	gga	aaa	gtg	aat	tct	1114

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_		gtg Val					-	_					_				1162
		ggt Gly					_					_			_		1210
	_	att Ile 390			-	_				_							1258
	_	tcg Ser	_				_	_		_			_				1306
		ctt Leu														j	1354
		cct Pro															1402
		tta Leu								_	-			_	_		1450
_		cgg Arg 470	_		_		_	_	_		_	_					1498
		ttg Leu															1546
		cca Pro		_	-				_		_						1594
		tgc Cys															1642
		cat His															1690
_	-	ccg Pro 550			_	_							_		_		1738
		tgc Cys															1786

											Gly ggg					1834
		_	_	_		_					gaa Glu		_		_	1882
				-			_				Gly ggg		_			1930
	-	_		_							agc Ser		_	_		1978
_	_		_	_	_	_	_	_			cac His 655					2026
											tgg Trp					2074
_			_		_			_	_		tca Ser			_	_	2122
_		Gly		_	_	_	_	_			acc Thr		_		_	2170
											cac His					2218
											gga Gly 735					2266
	Ala	His	Tyr	Leu	Asp	Lys		Val	Lys	Glu	ggt Gly	Cys	Pro	Gly	_	2314
-		-			-	_		_	-		aac Asn				_	2362
											gac Asp					2410
									_		gac Asp				_	2458
				-	_	_		_	_		tgc Cys 815			_		2506

					cct Pro 825	_		_	_			_		_		2554
					caa Gln											2602
					gat Asp											2650
					gcg Ala				-			_			_	2698
-					att Ile		_			_					_	2746
					att Ile 905		_	_	_		_		-	_		2794
				_	tct Ser	-		_	_			_				2842
		_			act Thr	-						_				2890
	_			_	atg Met	_		_			_			_	_	2938
_		_		_	gtg Val			_							_	2986
					agg Arg 985				_	_	_					3034
		-	_	ctg Leu 1000		_	a gaa 1 Glu			r I	tt co le Pi			hr Ā		3079
					cto Lev	_		_		a A.	ca gg la Gi			ys S		3124
_		aag Lys			Met		c caç Glr		_	1 1	ta co le Pi			sn L		3169
-	_	gtc Val		_	at <u>c</u> Met		g gcc L Ala	-	_		gg ag ly Ai	-			-	3214

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_				gcc Ala 1060	_			_	-		_				3259
				gca Ala 1075						tac Tyr		_			3304
				gtc Val 1090			-			_	_	_	_	_	3349
				aag Lys 1105					ttg Leu 1110						3394
-	_	_		atg Met 1120				_	_	_	_			_	3439
_	gac Asp	_	_	aac Asn 1135					aaa Lys 1140		aat Asn		-		3484
				cag Gln 1150	_		_		_	_	_		_		3529
				cgt Arg 1165	_					_	tgc Cys				3574
_	_			aaa Lys 1180		_	_					_	_		3619
	_		_	cta Leu 1195		_		_	ttc Phe 1200			_			3664
				ggg Gly 1210											3709
				cat His 1225											3754
	acg Thr			gtc Val 1240					tac Tyr 1245						3799
	_	-		tat Tyr 1255		_				_		_		_	3844
ctg	act	aaa	aac	gct	gaa	gtg	gtg	gca	ggg	acc	ggg	gaa	cag	tgc	3889

Leu	Thr	Lys	Asn	Ala 1270	Glu	Val	Val	Ala	Gly 1275	Thr	Gly	Glu	Gln	Cys 1280	
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				atg Met 1300											3979
				ttt Phe 1315											4024
				ata Ile 1330											4069
tca Ser	gct Ala	cga Arg	cct Pro	tta Leu 1345	acc Thr	tgt Cys	gat Asp	act Thr	agc Ser 1350	atg Met	cat His	atc Ile	agc Ser	cag Gln 1355	4114
				tgg Trp 1360							aac Asn				4159
				gtc Val 1375											4204
				gtc Val 1390											4249
				gtg Val 1405											4294
				tca Ser 1420							tcc Ser				4339
gtc Val	ctt Leu	tac Tyr	atc Ile	acg Thr 1435	gaa Glu	act Thr	gat Asp	gag Glu	aag Lys 1440	aag Lys	atc Ile	aac Asn	cga Arg	ata Ile 1445	4384
agg Arg	cag Gln	gtc Val	acg Thr	aca Thr 1450	gac Asp	Gly	gag Glu	atc Ile	tcc Ser 1455	tta Leu	gtg Val	gct Ala	Gly	ata Ile 1460	4429
cct Pro	tcg Ser	gaa Glu	tgt Cys	gac Asp 1465	tgc Cys	aag Lys	aac Asn	gac Asp	gcc Ala 1470	Asn	tgt Cys	gac Asp	tgc Cys	tac Tyr 1475	4474
				ggc Gly 1480						Lys					4519

		_	_	gcc Ala 1495	_		_			_			_	_	4564
				agg Arg 1510											4609
_			_	aac Asn 1525			_	_	-						4654
				ttt Phe 1540	_						_				4699
				ggt Gly 1555									agc Ser		4744
_		_	_	acc Thr 1570	_	_		-	_						4789
				gat Asp 1585											4834
				gtg Val 1600											4879
ctg Leu	aaa Lys	agc Ser	atg Met	acc Thr 1615	gct Ala	cag Gln	ggc	ctg Leu	gaa Glu 1620	ctg Leu	gtt Val	ttg Leu	ttt Phe	act Thr 1625	4924
	cat His			agt Ser 1630					acc Thr 1635				gaa Glu		4969
		Thr	Thr	ttt Phe 1645	Phe	Asp	Tyr	Asp	Ser				ctg Leu		5014
	_			ccc Pro 1660			-								5059
				atc Ile 1675											5104
				atc Ile 1690											5149
			_	caa Gln 1705					aac Asn 1710					ggg Gly 1715	5194

				ctt Leu 1720											5239
		_		gag Glu 1735			_	_	_		_	_			5284
				aga Arg 1750											5329
				tgg Trp 1765											5374
-		-		ggc Gly 1780		_									5 41 9
				ttt Phe 1795											5464
_	_			aaa Lys 1810			_		atc Ile 1815	_		_	_	_	5509
				ctc Leu 1825											5554
	_			tca Ser 1840					att Ile 1845		agc Ser				5599
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		Arg	Val	ttt Phe 1870	Ala	Asp	Gly	Lys	Thr	Trp	Ser	Tyr	Thr		5689
				atg Met 1885											5734
				gac Asp 1900											5779
				cgc Arg 1915											5824
				atc Ile											5869

				1930					1935					1940	
		-				-		_	ctt Leu 1950	_					5914
									aag Lys 1965						5959
									aca Thr 1980						6004
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									agg Arg 2010						6094
	_	_	_			_		_	gag Glu 2025	_		_	-		6139
									agc Ser 2040						6184
									ctg Leu 2055		att Ile				622
caç Glr	ttt Phe	gat Asp	gac Asp	atc Ile 2065	tct Ser	ggc Gly	aaa Lys	gtc Val	gag Glu 2070	cag Gln	ttt Phe	gga Gly	aaa Lys	ttc Phe 2075	627
									atc Ile 2085		tcc Ser				631
									cat His 2100						636
	caa Gln								atg Met 2115						640
	tat Tyr								aag Lys 2130						645
	g cct / Pro				Thr				gcg Ala 2145	Tyr					649
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				cgc Arg 2185							_	_	_	_	6634
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			_	act Thr 2230	_	_		_					tgg Trp	_	6769
				tac Tyr 2245					aga Arg 2250						6814
				cag Gln 2260											6859
		_	_	att Ile 2275			_		aac Asn 2280				tca Ser	_	6904
				tac Tyr 2290					gga Gly 2295						6949
				ggg Gly 2305					atc Ile 2310				aac Asn		6994
				gct Ala 2320											7039
cag Gln	acc Thr	cag Gln	tac Tyr	act Thr 2335	gcc Ala	tat Tyr	ggt Gly	gag Glu	atc Ile 2340	tac Tyr	ttt Phe	gac Asp	tcc Ser	aac Asn 2345	7084
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				gtg Val 2455											7444
				cag Gln 2470											7489
				aag Lys 2485											7534
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				ggc Gly 2515											7624
			Val	ctc Leu 2530	Asn	Ile	Ala	Asn	Glu	Asp					7669
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			tgg Trp	gca Ala 2650					cgc Arg 2655						8029
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				agt Ser 2710			ggc Gly	_		taa	ccc	cggg	gcc		8207
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125

120

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